

GenCore version 4.5
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OK protein - protein search, using sw model

Run on: January 7, 2002, 16:03:53 ; Search time 180.87 Seconds
(without alignments)
37,201 Million cell updates/sec

Title: US-08-569-749-7

Perfect score: 269
Sequence: 1 LARAGFYITGPGDRVACFAC.....MEPKDAMSEHRRHPNCPF 46

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: SP:REMBL.17:*
2: SP:archaea:*
3: SP:fungi:*
4: SP:human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	248	92.2	1140	09UNH1	09unh1 homo sapien
2	243	90.3	589	09QZC6	09qzc6 rattus norv
3	243	90.3	589	11 Q9ESB8	Q9ese8 rattus norv
4	236	87.7	602	11 Q9ESE9	Q9ese9 rattus norv
5	228	84.8	195	13 Q9IA70	Q9ia70 gallus gall
6	228	84.8	197	13 Q9IA69	Q9ia69 gallus gall
7	228	84.8	224	11 Q9H642	Q9h642 rattus norv
8	228	84.8	324	13 Q9PDN2	Q9pdn2 gallus gall
9	228	84.8	610	13 Q57319	Q57319 rattus norv
10	185	68.8	466	11 Q9ESR0	Q9esr0 rattus norv
11	185	68.8	501	11 Q9EQ05	Q9eq05 rattus norv
12	185	68.8	501	11 Q9EQ04	Q9eq04 rattus norv
13	141	52.4	597	11 Q9E015	Q9e015 mus musculu
14	133.5	49.6	4845	11 Q9E738	Q9e738 mus musculu
15	133.5	49.3	153	5 Q9YEM2	Q9yem2 drosophila
16	129	48.0	264	12 Q9YEM2	Q9yem2 amasacia moo
17	129	48.0	438	5 Q9YUX5	Q9yux5 drosophila
18	127	47.2	280	4 Q9HAP7	Q9hap7 homo sapien
19	127	47.2	298	4 Q9H2A8	Q9h2a8 homo sapien

20	126	46.8	261	12 Q9JES9	Q9jes9 epiphyas po
21	126	46.8	379	5 Q9U492	Q9u492 trichoplusi
22	125	46.5	276	12 Q9J744	Q9j744 buzura supp
23	123	45.7	268	12 Q9E232	Q9e232 helioverpa
24	123	45.7	268	12 Q9IF18	Q9if18 helioverpa
25	123	45.7	281	12 Q9YML8	Q9yml8 choristoneu
26	123	45.7	313	12 Q9J827	Q9j827 spodoptera
27	123	45.7	377	5 Q9N107	Q9n107 spodoptera
28	117	42.9	208	12 Q55770	Q55770 chilo litide
29	115.5	42.9	4904	5 Q9VH01	Q9vh01 drosophila
30	111	41.3	150	12 Q9YV4	Q9yv4 melanoplus
31	107	39.8	155	12 Q9YMI9	Q9ymi9 lymantria d
32	101.5	37.7	142	6 Q9GLN5	Q9gln5 sus scrofa
33	99.5	37.0	142	13 Q9DNK0	Q9dnk0 gallus gall
34	98	36.4	292	12 Q92394	Q92394 bombyx mori
35	97	36.1	281	12 Q9DV75	Q9dvt5 pluteia xy
36	92	34.2	284	12 Q9YK15	Q9yk15 epiphyas po
37	87.5	32.5	187	12 Q9DSW8	Q9dsw8 ascovirus d
38	85.5	31.8	285	12 Q9PY09	Q9pyq9 xestia c-ni
39	80	29.7	249	12 Q92435	Q92435 bombyx mori
40	80	29.7	301	12 Q9P254	Q9p254 trichoplusi
41	72	26.8	155	5 Q92837	Q92837 caenothabdi
42	72	26.8	317	12 Q9J849	Q9j849 spodoptera
43	70.5	26.2	137	4 Q9BV24	Q9bv24 homo sapien
44	66.5	24.7	329	12 Q9YV40	Q9yv40 melanoplus
45	65	24.2	87	11 Q09119	Q09119 mus musculu

ALIGNMENTS

RESULT 1
ID 09UNH1 PRELIMINARY; PRT: 1140 AA.
AC 09UNH1;
DT 01-MAY-2000 (TREMBLrel, 13, Created)
DT 01-MAY-2000 (TREMBLrel, 13, Last sequence update)
DE 01-JUN-2001 (TREMBLrel, 17, Last annotation update)
DE AP12-MLT FUSION PROTEIN.
CN AP12-MLT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-9272400; PubMed-10339464;
RA Dierlamm J., Baens M., Wlodarska I., Stefanova-Ouzounova M.,
Hernandez J.M., Hossfeld D.K., De Wolf-Peters C., Hagewilger A.,
Van den Bergh H., Marynen P.;
RT "The apoptosis inhibitor gene AP12 and a novel 18q gene, MLT, are
recurrently rearranged in the t(11;18)(q21;q21)pesassociated with
mucosa-associated lymphoid tissue lymphomas";
RT Blood 93:3601-3609(1999).
RL -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
CC EMBL: AF123094; AAD46161.1; -;
DR HSSP: AF13490; IOBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR003576; Caspase.
DR InterPro: IPR001309; ICE_p20.
DR InterPro: IPR003598; IG_C2.
DR InterPro: IPR003600; IG_Like.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00653; BIR_3.
DR Pfam: PF00047; Ig_2.
DR SMART: SM00238; BIR_3.
DR SMART: SM00115; CASC_1.
DR SMART: SM00408; IC2_1.
DR SMART: SM00410; IC_Like_1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS50208; CASPASE_P20; 1.

SEQ SEQUENCE 1140 AA: 128738 MW: 0C18D890287C723E CRC64;

Query Match 92.2%; Score 248; DB 11; Length 1140;
Best Local Similarity 91.3%; Pred. No. 3.3e-23;
Matches 42; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 LARAGFYITGPDGVACFCAGCGKLSNMEPKDAMSEHRRHPNCPF 46
119 LAKAGFYITGPDGVACFCAGCGKLSNMEPKDAMSEHRRHPNCPF 234

RESULT 2

090ZC6 PRELIMINARY; PRT: 589 AA.

AC 090ZC6: 01-MAR-2001 (TREMBLrel. 13, Created)
DT 01-MAR-2001 (TREMBLrel. 13, last sequence update)
DE INHIBITOR OF APOPTOSIS PROTEIN 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Dong Z., Denton M., Gu S.M., Sakumar P., Venkatchalam M.A.,
RT "Cloning of cDNA for rat inhibitor of apoptosis protein 2.";
RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.

CC -1 SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
DR EMBL: AF190020; AAF04585.1;
DR HSSP: Q13490; 1QBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; znf_fing.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
KW Zinc-finger.
SQ SEQUENCE 589 AA: 66777 MW: E6812FE3EA34142 CRC64;

Query Match 90.3%; Score 243; DB 11; Length 589;
Best Local Similarity 87.0%; Pred. No. 7.4e-23;
Matches 40; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 LARAGFYITGPDGVACFCAGCGKLSNMEPKDAMSEHRRHPNCPF 46
119 LAKAGFYITGPDGVACFCAGCGKLSNMEPKDAMSEHRRHPNCPF 221

RESULT 3

09SESE PRELIMINARY; PRT: 589 AA.

AC 09SESE: 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DE INHIBITOR OF APOPTOSIS PROTEIN 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Holcik M., Lefevre C.A., Hicks K., Korneluk R.G.;

RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of

Apoptosis Protein 1, 2, and 3 Genes.";
RT Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.

CC -1 SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
DR EMBL: AF183431; AAG22971.1;
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; znf_fing.
DR InterPro: IPR001315; CARD.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 1.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
KW Zinc-finger.
SQ SEQUENCE 589 AA: 66750 MW: B4F7089BD7CD285B CRC64;

Query Match 90.3%; Score 243; DB 11; Length 589;
Best Local Similarity 87.0%; Pred. No. 7.4e-23;
Matches 40; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 LARAGFYITGPDGVACFCAGCGKLSNMEPKDAMSEHRRHPNCPF 46
119 LAKAGFYITGPDGVACFCAGCGKLSNMEPKDAMSEHRRHPNCPF 221

RESULT 4

09SESE PRELIMINARY; PRT: 602 AA.

AC 09SESE: 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DE INHIBITOR OF APOPTOSIS PROTEIN 1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 1;
RP SEQUENCE FROM N.A.
RA Holcik M., Lefevre C.A., Hicks K., Korneluk R.G.;

RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of
Apoptosis Protein 1, 2, and 3 Genes.";
RT Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.

CC -1 SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
DR EMBL: AF183430; AAG22970.1;
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; znf_fing.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 1.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
KW Zinc-finger.
SQ SEQUENCE 602 AA: 67326 MW: CC91385E6A62DE5A CRC64;

Query Match 87.7%; Score 236; DB 11; Length 602;
Best Local Similarity 84.8%; Pred. No. 5.9e-22;
Matches 39; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 LARAGFYITGPDGVACFCAGCGKLSNMEPKDAMSEHRRHPNCPF 46
119 LAKAGFYITGPDGVACFCAGCGKLSNMEPKDAMSEHRRHPNCPF 234

[illegible]

	Query Match	84.8%	Score 228;	DB 13;	Length 197;	
	Best Local Similarity	80.4%;	Pred. No. 2e-21;			
Matches	37;	Conservative	5;	Mismatches	4;	Indels
						0;
Oy	1	LARAGFYITGPDYVACFACGGKLSMWEPKDAMSEHRHFPNCP	46			
		:				
Dd	51	LAKAGIYITGADKADKACFTCGGLDSMWEPKDNASEHRHFPNCP	96			
RESULT	7					
088642		PRELIMINARY:	PRT:	224 AA.		
AC	088642:					
DT	01-NOV-1998 (TREMBLrel_08, Created)					
RT	01-NOV-1998 (TREMBLrel_08, Last sequence update)					
DT	01-JUN-2001 (TREMBLrel_17, Last annotation update)					
DE	INHIBITOR OF APOPTOSIS PROTEIN (FRAGMENT).					
GN	RAP1.					
OS	Rattus norvegicus (Rat).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.					
OX	NCBL_TaxId=10116;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=MISTAR; TISSUE=OVARY; CORPUS LUTEUM;					
RA	Bradley C.K., Lareu R.R., Dharmarajan A.M.;					
RT	"Cloning and characterisation of an inhibitor of apoptosis protein					
(IAP) in the rat corpus luteum."						
RL	Submitted (Aug-1998) to the EMBL/GenBank/DDB databases.					
DR	EMBL: AF081503; AAC32497.1; "					
DR	HSSP: OJ3490; IOBH.					
DR	InterPro: IPR001370; BIR.					
DR	Pfam: PF00653; BIR: 2.					
DR	SMART: SM00238; BIR: 2.					
DR	PROSITE: PS50143; BIR_REPEAT_2; 3.					
NON_TER	1					
FT	NON_TER	224				
SQ	SQIDENCE	224 AA: 25209 MW; 213A52534D5E56A CRC64;				
Query Match		84.8%; Score 228; DB 11; Length 224;				
Best Local Similarity		80.4%; Pred. No. 2.3e-21;				
Matches	37;	Conservative	3;	Mismatches	6;	Indels
						0;
Gy	1	LARAGFYITGPDYVACFACGGKLSMWEPKDAMSEHRHFPNCP	46			
		:				
Dd	105	LGRAAFYITGPDYVACFACGGKLSMWEPNDLLSEHRHFPNCP	150			
RESULT	8					
09DDN2		PRELIMINARY:	PRT:	324 AA.		
ID	09DDN2:					
AC	09DDN2:					
DT	01-MAR-2001 (TREMBLrel_16, Created)					
RT	01-MAR-2001 (TREMBLrel_16, Last sequence update)					
DT	01-JUN-2001 (TREMBLrel_17, Last annotation update)					
DE	APOPTOSIS INHIBITOR CH-IAP1 (FRAGMENT).					
OS	Gallus gallus (Chicken).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
CC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;					
OX	Gallus					
NCBI_TaxId=9031;						
[1]						
RP	SEQUENCE FROM N.A.					
RA	Fendler C.N., Bargmann W.J., Varadarajan J., Rose H.R. Jr.;					
RT	"The apoptosis inhibitor ch-iap1 is a direct transcriptional target of					
v-rel and c-rel."						
RL	Submitted (Oct-2000) to the EMBL/GenBank/DDB databases.					
DR	EMBL: AF311289; AAG42316.1; "					
DR	InterPro: IPR001370; BIR.					
DR	Pfam: PF00653; BIR: 3.					
DR	SMART: SM00238; BIR: 3.					
DR	PROSITE: PS01282; BIR_REPEAT_1; 1					

DR pfam: PF00653; BIR: 3.
DR pfam: PF00097; ZF-C3HC4; 1.
DR SMART: SM00238; BIR: 3.
DR SMART: SM00184; RING: 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 1.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
KW Zinc-finger.
SQ SEQUENCE 501 AA; 56548 MW; 0973FBF28E81C5A0 CRC64;

Query Match
Best Local Similarity 71.7%; Score 185; DB 11; Length 501;
Matches 33; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

OY 1 LARAGFYIGDGVACGKLSNWKPKDAMSEHRHPPNCPF 46
DB 184 LSAAGLYTGIDVQVCGCGKLNWPKDAMSEHRHPPNCPF 229

RESULT 12
ID Q9B004 PRELIMINARY; PRT; 501 AA.
AC Q9B004;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE INHIBITOR OF APOPTOSIS PROTEIN 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MISTAR; TISSUE=OVARY;
RA Lareu R.R., Bradley C.K., Lacher M., Ellis R.R., Dharmarajan A.M.;
RT Cloning, characterization and regulation of an inhibitor of apoptosis
protein in the rat corpus luteum.
RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
RC -1 SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
DR EMBL: AF043344; AAC41193.1;
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_rlng.
DR pfam: PF00653; BIR: 3.
DR SMART: SM00238; BIR: 3.
DR SMART: SM00184; RING: 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 1.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
KW Zinc-finger.
SQ SEQUENCE 501 AA; 56578 MW; 4863F69FF2E0C8CD CRC64;

Query Match
Best Local Similarity 71.7%; Score 185; DB 11; Length 501;
Matches 33; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

OY 1 LARAGFYIGDGVACGKLSNWKPKDAMSEHRHPPNCPF 46
DB 184 LSAAGLYTGIDVQVCGCGKLNWPKDAMSEHRHPPNCPF 229

RESULT 13
ID Q9R015 PRELIMINARY; PRT; 597 AA.
AC Q9R015;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE NEURONAL APOPTOSIS INHIBITORY PROTEIN.
GN BIRCIE OR NAIP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99431676; PubMed=10501978;
RA Huang S., Schaff J.M., Gromey J.D., Endlitz M.G., Dietrich W.F.;
RT "The mouse Naip gene cluster on Chromosome 13 encodes several distinct
functional transcripts."
RL Mamm. Genome 10:1032-1035(1999).
DR EMBL: AF135493; AAD56765.1;
DR HSSP: Q13490; 10BH.
DR MGD: MGI:1298220; Bircie.
DR InterPro: IPR001370; BIR.
DR pfam: PF00653; BIR: 3.
DR SMART: SM00238; BIR: 3.
DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
SQ SEQUENCE 597 AA; 68322 MW; 4042E36E51A7F9A0 CRC64;

Query Match
Best Local Similarity 52.4%; Score 141; DB 11; Length 597;
Matches 24; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

OY 1 LARAGFYIGDGVACGKLSNWKPKDAMSEHRHPPNCPF 46
DB 135 LSAAGVFTGKRDVQVCGCGSIGNWEEDDPWKHAKWPKCF 180

RESULT 14
ID O88738 PRELIMINARY; PRT; 4845 AA.
AC O88738;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE UBIQUITIN-CONJUGATING ENZYME.
GN BIRC6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98292517; PubMed=9628897;
RA Houser H.P., Bardoff M., Pyrochajski G., Jentsch S.;
RT "A giant ubiquitin-conjugating enzyme related to IAP apoptosis
inhibitors."
RL J. Cell Biol. 141:1415-1422(1998).
CC -1- FUNCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUITIN TO OTHER
PROTEINS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + UBIQUITIN + PROTEIN LYSINE - AMP +
PYROPHOSPHATE + PROTEIN N-UBIQUITYLlysine.
CC -1- PATHWAY: SECOND STEP IN UBIQUITIN CONJUGATION.
CC -1- MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-
THIOLESTER FORMATION (BY SIMILARITY).
CC -1- SIMILARITY: TO UBIQUITIN-CONJUGATING ENZYMS DOMAIN.
DR EMBL: Y17267; CAA76720.1;
DR HSSP: Q13490; 10BH.
DR MGD: MGI:1276108; Birc6.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR00608; UBO_conjugat.
DR pfam: PF00653; BIR: 1.
DR pfam: PF00179; UO_conj; 1.
DR SMART: SM00238; BIR: 1.
DR SMART: SM00212; UBCe; 1.
DR PROSITE: PS0143; BIR_REPEAT_2; 1.
DR PROSITE: PS0127; UBIQUITIN_CONJUGAT_2; 1.
KW Lysase; Ubiquitin conjugation.
SQ SEQUENCE 4845 AA; 528418 MW; 35C585F73B8CF94C CRC64;

Query Match
Best Local Similarity 49.6%; Score 133.5; DB 11; Length 4845;
Matches 51.0%; Pred. No. 5.6e-08;
